

SEQUENCE LISTING

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TECH CENTER 1600/2300

(1) GENERAL INFORMATION:

(i) APPLICANT: Beach, David H.
Demetrick, Douglas J.
Serrano, Manuel
Hannon, Gregory J.

(ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
Uses Related Thereto

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Boston
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPad

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/016,869
(B) FILING DATE: 30-JAN-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/893,274
(B) FILING DATE: 15-JUL-1994

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 14-SEP-1994

(vii) PRIOR APPLICATION DATA:

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/227,371
(B) FILING DATE: 14-APR-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/154,915
(B) FILING DATE: 18-NOV-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/991,997
(B) FILING DATE: 17-DEC-1992

Revised per Amst. I

Q1

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: MIV-071.10

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 994 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 41..508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC	ATG GAT CCG GCG GCG	55
	Met Asp Pro Ala Ala	
	1 5	
GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCC	103	
Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala		
	10 15 20	
CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG	151	
Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu		
	25 30 35	
CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG	199	
Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met		
	40 45 50	
ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG	247	
Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu		
	55 60 65	
CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT	295	
Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala		
	70 75 80 85	
GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG	343	
Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly		
	90 95 100	
GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG	391	
Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu		
	105 110 115	
GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT	439	
Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala		
	120 125 130	
GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA	487	
Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu		
	135 140 145	
GGT CCC TCA GAC ATC CCC GAT TGAAAGAACC AGAGAGGCTC TGAGAAACCT	538	
Gly Pro Ser Asp Ile Pro Asp		

150	CGGGAAACTT	AGATCATCAG	TCACCGAAGG	TCCTACAGGG	CCACAACTGC	CCCCGCCACA	598
	ACCCACCCCG	CTTTCGTAGT	TTTCATTTAG	AAAAATAGAGC	TTTTAAAAAT	GTCCTGCCTT	658
	TTAACGTAGA	TATAAGCCTT	CCCCCACTAC	CGTAAATGTC	CATTTATATC	ATTTTTTATA	718
	TATTCTTATA	AAATGTAA	AAAGAAAAAC	ACCGCTTCTG	CCTTTTCACT	GTGTTGGAGT	778
	TTTCTGGAGT	GAGCACTCAC	GCCCTAAGCG	CACATTCATG	TGGGCATTTT	TTGGCAGCCT	838
	CGCAGCCTCC	GGAAGCTGTC	GACTTCATGA	CAAGCATTTT	GTGAACTAGG	GAACTCAGG	898
	GGGGTTACTG	GCTTCTCTTG	AGTCACACTG	CTAGCAAATG	GCAGAACCAA	AGCTCAAATA	958
	AAAAATAAAAT	TATTTTCATT	CATTCACTCA	AAAAAA			994

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Pro	Ala	Ala	Gly	Ser	Ser	Met	Glu	Pro	Ser	Ala	Asp	Trp	Leu
1				5					10					15	
Ala	Thr	Ala	Ala	Ala	Arg	Gly	Arg	Val	Glu	Glu	Val	Arg	Ala	Leu	Leu
			20					25					30		
Glu	Ala	Val	Ala	Leu	Pro	Asn	Ala	Pro	Asn	Ser	Tyr	Gly	Arg	Arg	Pro
		35				40						45			
Ile	Gln	Val	Met	Met	Met	Gly	Ser	Ala	Arg	Val	Ala	Glu	Leu	Leu	Leu
	50					55					60				
Leu	His	Gly	Ala	Glu	Pro	Asn	Cys	Ala	Asp	Pro	Ala	Thr	Leu	Thr	Arg
65					70					75					80
Pro	Val	His	Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val	Val
				85					90					95	
Leu	His	Arg	Ala	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly	Arg
			100					105				110			
Leu	Pro	Val	Asp	Leu	Ala	Glu	Glu	Leu	Gly	His	Arg	Asp	Val	Ala	Arg
		115				120					125				
Tyr	Leu	Arg	Ala	Ala	Ala	Gly	Gly	Thr	Arg	Gly	Ser	Asn	His	Ala	Arg
	130					135					140				
Ile	Asp	Ala	Ala	Glu	Gly	Pro	Ser	Asp	Ile	Pro	Asp				
145				150						155					

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 328..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGGACTCCG CGACGGTCCG CACCCTGCGG CCAGAGCGGC TTTGAGCTCG GCTGCTTCCG 60
 CGCTAGGCGC TTTTTCCTCAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGCGCCAGGA 120
 AAAGCCCGGA GCTAACGACC GGCCGCTCGG CACTGCACGG GGCCCAAGC CGCAGAAAGAA 180
 GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTGCGCCCG 240
 AGCAGCGTGG GAAAGAAGGG AAGAGTGTCG TTAAGTTTAC GGCCAACGGT GGATATATCCG 300
 GGCCGCTGCG CGTCTGGGGG CTGCGGA ATG CGC GAG GAG AAC AAG GGC ATG 351

Met Arg Glu Glu Asn Lys Gly Met

CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA 399
 Pro Ser Gly Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly
 10 15 20
 CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC 447
 Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn
 25 30 35 40
 GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC 495
 Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly
 45 50 55
 AGC GCC CGC GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG CCC AAC 543
 Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn
 60 65 70
 TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG 591
 Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg
 75 80 85
 GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG GCG CGG 639
 Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg
 90 95 100
 CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG 687
 Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu
 105 110 115 120
 GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG 735
 Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly
 125 130 135
 GAC TGACGCCAGG TTCCCAGCC GCCACAACG ACTTTATTTT CTTACCCAAT
 Asp

TTCCCACCCC CACCCACCTA ATTCGATGAA GGOTGCCAAC GGGGAGCGG

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu
 1 5 10 15
 Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
 20 25 30
 Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
 35 40 45
 Ala Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu
 50 55 60
 Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr

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65		70		75		80									
Arg	Pro	Val	His	Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val
			85						90					95	
Val	Leu	His	Arg	Ala	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly
		100					105					110			
Arg	Leu	Pro	Val	Asp	Leu	Ala	Glu	Glu	Arg	Gly	His	Arg	Asp	Val	Ala
		115				120						125			
Gly	Tyr	Leu	Arg	Thr	Ala	Thr	Gly	Asp							
	130					135									

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 853 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 213..587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAGTACAGC	AGCGGGAGCA	TGGGTCGCAG	GTTCTTGGTC	ACTGTAAGGA	TTCAGCGCGC	60
GGGCCGCCCA	CTCCAAGAGA	GGGTTTTCTT	GGTGAAGTTC	GTGCGATCCC	GGAGACCCAG	120
GACAGCGAGC	TGCGCTCTGG	CTTTCGTGAA	CATGTTGTTG	AGGCTAGAGA	GGATCTTGAG	180
AAGAGGGCCG	CACCGGAATC	CTGGACCAGG	TG ATG	ATG ATG	GGC AAC	GTT CAC
			Met Met	Met Gly	Asn Val	His
			1		5	
GTA GCA	GCT CTT	CTG CTC	AAC TAC	GGT GCA	GAT TCG	AAC TGC
Val Ala	Ala Leu	Leu Leu	Asn Tyr	Gly Ala	Asp Ser	Asn Cys
	10		15		20	
CCC ACT	ACC TTC	TCC CGC	CCG GTG	CAC GAC	GCA GCG	CGG GAA
Pro Thr	Thr Phe	Ser Arg	Pro Val	His Asp	Ala Ala	Arg Glu
	25		30		35	
CTG GAC	ACG CTG	GTG GTG	CTG CAC	GGG TCA	GGG GCT	CGG CTG
Leu Asp	Thr Leu	Val Val	Leu His	Gly Ser	Gly Ala	Arg Leu
	40		45		50	
CGC GAT	GCC TGG	GGT CGC	CTG CCG	CTC GAC	TTG GCC	CAA GAG
Arg Asp	Ala Trp	Gly Arg	Leu Pro	Leu Asp	Leu Ala	Gln Glu
	60		65		70	
CAT CAA	GAC ATC	GTG CGA	TAT TTG	CGT TCC	GCT GGG	TGC TCT
His Gln	Asp Ile	Val Arg	Tyr Leu	Arg Ser	Ala Gly	Cys Ser
	75		80		85	
TCC GCT	GGG TGG	TCT TTG	TGT ACC	GCT GGG	AAC GTC	GCC CAG
						ACC GAC
						521

Ser	Ala	Gly	Trp	Ser	Leu	Cys	Thr	Ala	Gly	Asn	Val	Ala	Gln	Thr	Asp	
	90						95					100				
GGG	CAT	AGC	TTC	AGC	TCA	AGC	ACG	CCC	AGG	GCC	CTG	GAA	CTT	CGC	GGC	569
Gly	His	Ser	Phe	Ser	Ser	Ser	Thr	Pro	Arg	Ala	Leu	Glu	Leu	Arg	Gly	
	105					110					115					
CAA	TCC	CAA	GAG	CAG	AGC	TAAATCCGCC	TCAGCCCGCC	TTTTTCTTCT								617
Gln	Ser	Gln	Glu	Gln	Ser											
	120				125											
TAGCTTCACT	TCTAGCGATG	CTAGCGTGTC	TAGCATGTGG	CTTTAAAAAA	TACATAATAA											677
TGCTTTTTTTT	GCAATCACGG	GAGGGAGCAG	AGGGAGGGAG	CAGAAGGAGG	GAGGGAGGGA											737
GGGAGGGACC	TGGACAGGAA	AGGAATGGCA	TGAGAACTG	AGCGAAGGCG	GCCGCGAAGG											797
GAATAATGGC	TGGATTGTTT	AAAAAAATAA	AATAAAGATA	CTTTTAAAAA	TGTCAA											853

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Met	Met	Gly	Asn	Val	His	Val	Ala	Ala	Leu	Leu	Leu	Asn	Tyr	Gly	
1				5				10						15		
Ala	Asp	Ser	Asn	Cys	Glu	Asp	Pro	Thr	Thr	Phe	Ser	Arg	Pro	Val	His	
			20					25					30			
Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val	Val	Leu	His	Gly	
			35				40					45				
Ser	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly	Arg	Leu	Pro	Leu	
	50					55					60					
Asp	Leu	Ala	Gln	Glu	Arg	Gly	His	Gln	Asp	Ile	Val	Arg	Tyr	Leu	Arg	
	65				70				75					80		
Ser	Ala	Gly	Cys	Ser	Leu	Cys	Ser	Ala	Gly	Trp	Ser	Leu	Cys	Thr	Ala	
				85					90					95		
Gly	Asn	Val	Ala	Gln	Thr	Asp	Gly	His	Ser	Phe	Ser	Ser	Ser	Thr	Pro	
		100					105						110			
Arg	Ala	Leu	Glu	Leu	Arg	Gly	Gln	Ser	Gln	Glu	Gln	Ser				
		115				120						125				

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCA CTC CTG GAA GCC GGC GCA GAT CCC AAC GCC CTG AAC CGC TTC GGG	48
Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly	
1 5 10 15	
AGG CGC CCA ATC CAG GTC ATG ATG ATG GGC AGC GCC AGG GTG GCA GAG	96
Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu	
20 25 30	
CTG CTG CTG CTC CAC GGA GCA GAA CCC AAC TGC GCC GAC CCT GCC ACC	144
Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr	
35 40 45	
CTT ACC AGA CCT GTG CAC GAC GCA GCT CGG GAA GGC TTC CTG GAC ACG	192
Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr	
50 55 60	
CTT GTC GTG CTG CAC CGG GCA GGG GCG CGG TTG GAT GTG	231
Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val	
65 70 75	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly	
1 5 10 15	
Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu	
20 25 30	
Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr	
35 40 45	
Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr	
50 55 60	
Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val	
65 70 75	

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
 1 5 10 15
 Tyr Gly Thr Val Tyr Lys Ala Xaa Asp Pro His Ser Gly His Phe Val
 20 25 30
 Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly
 35 40 45
 Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
 50 55 60
 Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
 65 70 75 80
 Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
 85 90 95
 Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu
 100 105 110
 Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu
 115 120 125
 Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu
 130 135 140
 Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly
 145 150 155 160
 Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val
 165 170 175
 Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala
 180 185 190
 Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe
 195 200 205
 Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly
 210 215 220
 Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg
 225 230 235 240

Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro
 245 250 255
 Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu
 260 265 270
 Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg
 275 280 285
 Ala Leu Gln His Ser Tyr Leu His Lys Asp Glu Gly Asn Pro Glu
 290 295 300

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Glu Lys Asp Gly Leu Cys Arg Ala Asp Gln Gln Tyr Glu Cys Val
 1 5 10 15
 Ala Glu Ile Gly Glu Gly Ala Tyr Gly Lys Val Phe Lys Ala Xaa Asp
 20 25 30
 Leu Lys Asn Gly Gly Arg Phe Val Ala Leu Lys Arg Val Arg Val Gln
 35 40 45
 Thr Gly Glu Glu Gly Met Pro Leu Ser Thr Ile Arg Glu Val Ala Val
 50 55 60
 Leu Arg His Leu Glu Thr Phe Glu His Pro Asn Val Val Arg Leu Phe
 65 70 75 80
 Asp Val Cys Thr Val Ser Arg Thr Asp Arg Glu Thr Lys Leu Thr Leu
 85 90 95
 Val Phe Glu His Val Asp Gln Asp Leu Thr Thr Tyr Leu Asp Lys Val
 100 105 110
 Pro Glu Pro Gly Val Pro Thr Glu Thr Ile Lys Asp Met Met Phe Gln
 115 120 125
 Leu Leu Arg Gly Leu Asp Phe Leu His Ser His Arg Val Val His Arg
 130 135 140
 Asp Leu Lys Pro Gln Asn Ile Leu Val Thr Ser Ser Gly Gln Ile Lys
 145 150 155 160

Leu Ala Asp Phe Gly Leu Ala Arg Ile Tyr Ser Phe Gln Met Ala Leu
165 170 175

Thr Ser Val Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu
180 185 190

Gln Ser Ser Tyr Ala Thr Pro Val Asp Leu Trp Ser Val Gly Cys Ile
195 200 205

Phe Ala Glu Met Phe Arg Arg Lys Pro Leu Phe Arg Gly Ser Ser Asp
210 215 220

Val Asp Gln Leu Gly Lys Ile Leu Asp Val Ile Gly Leu Pro Gly Glu
225 230 235 240

Glu Asp Trp Pro Arg Asp Val Ala Leu Pro Arg Gln Ala Phe His Ser
245 250 255

Lys Ser Ala Gln Pro Ile Glu Lys Phe Val Thr Asp Ile Asp Glu Leu
260 265 270

Gly Lys Asp Leu Leu Leu Lys Cys Leu Thr Phe Asn Pro Ala Lys Arg
275 280 285

Ile Ser Ala Tyr Ser Ala Leu Ser His Pro Tyr Phe Gln Asp Leu Glu
290 295 300

Arg Cys Lys Glu Asn Leu Asp Ser His Leu Pro Pro Ser Gln Asn Thr
305 310 315 320

Ser Glu Leu Asn Thr Ala
325

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
1 5 10 15

Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
 35 40 45
 Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
 50 55 60
 Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
 65 70 75 80
 Arg Xaa Ala Xaa Gly
 85

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
 1 5 10 15
 Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
 20 25 30
 Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
 35 40 45
 Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu
 50 55 60
 Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa
 65 70 75 80
 Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
 85 90 95
 Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
 100 105 110
 Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa
 115 120 125
 Xaa Tyr Leu Arg Xaa Ala Xaa Gly Gly Thr Arg Gly Ser Asn His Ala
 130 135 140
 Arg Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp

145

150

155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Arg	Glu	Glu	Asn	Lys	Gly	Met	Pro	Ser	Gly	Gly	Gly	Ser	Asp	Glu	1	5	10	15
Gly	Leu	Ala	Thr	Pro	Ala	Arg	Gly	Leu	Val	Glu	Lys	Val	Arg	His	Ser	20	25	30	
Trp	Glu	Ala	Gly	Ala	Asp	Pro	Asn	Gly	Val	Asn	Arg	Phe	Gly	Arg	Arg	35	40	45	
Ala	Ile	Gln	Val	Met	Met	Met	Gly	Xaa	Xaa	Xaa	Val	Ala	Xaa	Leu	Leu	50	55	60	
Leu	Xaa	Xaa	Gly	Ala	Xaa	Xaa	Asn	Cys	Xaa	Asp	Pro	Xaa	Thr	Xaa	Xaa	65	70	75	80
Xaa	Arg	Pro	Val	His	Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	85	90	95	
Val	Val	Leu	His	Xaa	Xaa	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	100	105	110	
Gly	Arg	Leu	Pro	Xaa	Asp	Leu	Ala	Xaa	Glu	Xaa	Gly	His	Xaa	Asp	Xaa	115	120	125	
Xaa	Xaa	Tyr	Leu	Arg	Xaa	Ala	Xaa	Gly	Asp	130	135								

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Met	Met	Gly	Xaa	Xaa	Xaa	Val	Ala	Xaa	Leu	Leu	Leu	Xaa	Xaa	Gly	1	5	10	15
Ala	Xaa	Xaa	Asn	Cys	Xaa	Asp	Pro	Xaa	Thr	Xaa	Xaa	Xaa	Arg	Pro	Val	20	25	30	
His	Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val	Val	Leu	His	35	40	45	
Xaa	Xaa	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly	Arg	Leu	Pro	50	55	60	
Xaa	Asp	Leu	Ala	Xaa	Glu	Xaa	Gly	His	Xaa	Asp	Xaa	Xaa	Xaa	Tyr	Leu	65	70	75	80
Arg	Xaa	Ala	Xaa	Gly	Cys	Ser	Leu	Cys	Ser	Ala	Gly	Trp	Ser	Leu	Cys	85	90	95	
Thr	Ala	Gly	Asn	Val	Ala	Gln	Thr	Asp	Gly	His	Ser	Phe	Ser	Ser	Ser	100	105	110	
Thr	Pro	Arg	Ala	Leu	Glu	Leu	Arg	Gly	Gln	Ser	Gln	Glu	Gln	Ser		115	120	125	

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val	Ala	Glu	Ile	Gly	Xaa	Gly	Ala	Tyr	Gly	Xaa	Val	Xaa	Lys	Ala	Arg	Asp	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Xaa Lys Ala Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ala Arg Asp
1

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 960 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAGAGGGA ATTTCGGCACGA GGCAGCATG GAGCCTTCGG CTGACTGGCT GGCCACGGCC	60
GCGGCCCGGG GTCGGGTAGA GGAGGTGCGG GCGCTGCTGG AGGCGGTGGC GCTGCCCCAA	120
CGCACC GAAT AGTTACGGTC GGAGGCCGAT CCAGGTCATG GATGATGGGC AGCGCCCCGA	180
GTGGCGGAGC TGCTGCTGCT CCACGGGCGG GAGCCCCAACT GCGCCGACCC CGCCACTCTC	240
ACCCGACCCG TGCACCACGC TGCCCGGGAG GGCTTCTGGA CACGCTGGTG GTGCTGCACC	300
GGGCCGGGGC GCGGCTGGAC GTGCGCGATG CCTGGGGCCG TCTGCCCCGTG GACCTGGCTG	360
AGGAGCTGGG CCATCGCGAT GTCGCACGGT ACCTGCGCGC CCGTGCGGGG GGCACCAGAG	420

GCAGTAACCA TGCCCGCATA GATGCCGCGG AAGGTCCCTC AGACATCCCC GATTGAAAGA	480
ACCAGAGAGG CTCTGAGAAA CCTCGGGAAA CTTAGATCAT CAGTCACCGA AGGTCCTACA	540
GGGCCACAAC TGCCCCCGCC ACAACCCACC CCGCTTTCGT AGTTTTTCATT TAGAAAATAG	600
AGCTTTTAAA AATGTCCTGC CTTTAAACGT AGATATAAGC CTTCCCCCAC TACCGTAAAT	660
GTCCATTTAT ATCATTTTTT ATATATTCTT ATAAAAATGT AAAAAAAGAA AAACACCGCT	720
TCTGCCTTTT CACTGTGTTG GAGTTTCTG GAGTGAGCAC TCACGCCCTA AGCGCACATT	780
CATGTGGGCA TTTCTTGCGA GCCTCGCAGC CTCCGGAAGC TGTCGACTTC ATGACAAGCA	840
TTTTGTGAAC TAGGGAAGCT CAGGGGGGTT ACTGGCTTCT CTTGAGTCAC ACTGCTAGCA	900
AATGGCAGAA CCAAAGCTCA AATAAAAATA AAATTATTTT CATTCAATTCA CTCAAAAAAA	960

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGNGGNAAGN TGTGGGGGAA AGTTTGGGGA TGGAANACCA ANCCCTCCTT TCNTTACCAA	60
ACNCTGGCTC TGNCGAGGCT NCNTCCGANT GGTNCCOCCG GGGGAGACCC AACCTGGGNC	120
GACTTCAGGG NTGCNACATT CATTCACTAA GTGCTNGGAG NTAATANCAC CTCCTCCGAG	180
CANNACAGG NTCGGAGGGG GCTCTTCCCC CACCACCGGA GGAAGAAAGA GGAGGGNCTN	240
CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATGGATCCGG CGGCGGGGAG	300
CAGCATGGAN CTTTCGACTG ACTGACTGCC TCGC	334

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCNCTTATTG NTAGGANATA ATAACACCTC CACCGATAAC TTCACTTACA ACGTCCCNNT 60
TCCTGGAAAG ATACACAGCG TTCCCTCCAG AGGATTGTG GGACAGGGTN GGAGNGGTCT 120
CTTCCNCCAC CACCGGAGGA AGAAAGAGGA GGGGCTGNCT GTTCACCAGA GGGTGGGACG 180
GACCNCGTAC GCTCGNCGNC TNCGGAGAGG GGGAGAGCAT CANCGNCGN CGGGGAGCAA 240
CATGGAACCG NCGGCGGGGA GCAGCATGGA NCCTTCGGCT GACTGGCTGN CCACGNCCAC 300
GNCCCGGGGT CGGGTAGAGG AGGTGCGGNC GCTNCTGGAG GCGGGGNCTC TGNCCAACNC 360
GCTAAAN 368

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 404 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACNNNCTCC GGCCGGNGTC GGGTAGAGGA GGTGCGGCG CTGCTGGAGG CGGGGGCGCT 60
GCCCAACGCA CCGAATAGTT ACGGTCGGAG GCCGATCCAG GTNNGGGTAG AGGGTCTGCA 120
GCGGGAGCAG GGGATGGCGG GCGACTCTGG AGGACGAAGT TTGCAGGGGA ATTGGAATCA 180
GGTAGCGCTT CGATTCTCCN GAAAAGGGG AGGCTTCCTG GGGAGTTTTC AGAAGGGGTT 240
TGTAATCACA GACCTCCTCC TGGCGACGTC CTGGGGGCTT GGAAGCCAA GGAAGAGGAA 300
TNAGGAGCCA CGCGGTACG AGTCTCTCGA ATGCTGAGAA GATCTNAAGG GGGGAACATA 360
TTTGTATTAG CNTCCAAGTN TNCTCTNAT CANATACAAA NTNC 404

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCTNANCCC GGGTAGAGGG TCTGCAGCGG GAGCAGNGGA TGGCGGGCGA CTCTGCAGGA	60
CGAAGTTGGC AGGGGAATTG GAATCAGGTA GCGCTTCGAN TCTCCGAAA AAGGGGAGGC	120
TTCCTGGGGA GTTNNCAGAA GGGGTTTGTA ATCACAGNCC TCCNCCTGGC GACGCCCTGG	180
GGGGTTGGGA AGCCAAGGAA GAGGAATGAG GAGNCACGCG CNTACAGNTC TCTCGAATNC	240
TGANAAGATC TGAAGGGGGG AACATATTTG TATTAGNATN NAAGTATGCT CTTTATCAGA	300
TAGAAAATTC ACGAACGTGT GGNATAAAAA GGGAGTCTTA AAGAAATNTA AGATGTGCTG	360
GGACTACTTA GCCTCCAANA CACAGATNCC TGGATGGAGC T	401

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAAANNAAAA AAAATCTCCC AGGCCTAACA TAATTNTCAG GAAAGAAATT TCAGTAGTTG	60
NATCTCAGGG GAAATACAGG AAGTTAGCCT GGAGTAAAG TCAGTGTGTC CCTGCCCCCTT	120
TGCTANATTG CCCGTGCCTC ACAGTGCTCT CTGCCTGTGA CGACAGCTCC NCAGAAGTTC	180
GGAGGATATA ATGGAATTCA TTGTGTACTG AAGAAATGGAT AGAGAACTCA AGAAGGAAAT	240
TGGAAACTGG AAGCAAATGT AGGGGTAATT AGACACCTGG GGCTTCTGTG GGGGTCTGCT	300
TGGCGGTGAG GGGGCTCTAC ACAAGCTTCC TTTCCGTCAT GCCGNCCCCC ACCCTGGCTC	360
TGACCATTCT GTTCTCTCTG GCAGGTCATG ATGATGGGCA GCGCCCGAGG CGCGGAGCTG	420
CTGCTGCTCC ACGGCGCGGA GCCCACTGCT CCGACGCCG	459

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AANAAAAAAG AAATNGATAA NATAGAGGAA TGAACANATT AAAATCAAAA AACANAACAN	60
AGACATAATA AAAAACGAGA ATGTTCTAGA CNTAATCATA ATTATAAAGC TCAAGACTCA	120
TTGATATNAA GGADATTGAA GGGAAATCTT AACTAGCACA ANNGNATNAA AAAANAATTC	180
CCACGACACC GCCACTCTCA ACGCATCCGT GCTCGACACT GCCCGGGAGG TCNTCCTGGA	240
CACGCTGGTG GTNCTCCACC GGNCCGGGGC ACGTCTGGAC GTGCGCGATG COTGGGNCCG	300
NCTACCCGTG GTACCTGACT GAGGACCTGG GCCATCCCGA TTTCGCNGGG TANTCNGNG	360
GGCTGNNGGGG GCCAANAGAG GNCANTACCC	390

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 214 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCTGCNACGA CCCCGCCACT CTCACCCGAC CCGTGACGA CGCTGTCCGG GAGGGTTTCC	60
TGGACACGCT GGTGGTGCTG CACCGGGCCG GGGNGCGGTT GGACGTGCGC GATGCCTGGG	120
GCCGCCTNCC CGTGGNACCT GGTGAGGAG CTGGGNCATC GCGATGTCGC ACGGTACCTG	180
CGCGCGTTGC GGGGGGCACC AGAGGNNAGT NACC	214

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

NCTCTCACGG TGGGGAGGCC AACTGCGCCG AACCCGCCAC TCTCACCCGA CCCGCGCACG	60
ACGGTGCCCG GGAGGGGTTC CTGGACACGC TGGTGGTGCT GCACCGGGCC GGGGCGCGGC	120
TGGACGTTTCG NGATGCCTGG GGGNTCTNTC CGTNGNACCT GGCTGAAGAG CTGGNNCATC	180
GNGATGTCGC ACGGCCNCTG TGTGNGGNTG CGGGGGGCAC CATAGGTCAG TNTCC	235

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NAAGTATGAG CGAAACNAAT TGTGGTTTGA GAANAGGNAA TCGTAGGGAA CTTCGGGATC	60
CCNCNGGGAN CNCCAGAACC TGAGNCGCCN ATTGGAAATN ACAAAGTNC TGNATCACTC	120
CGNACCAGGT NCAAAAGATA CCTGGGGANG CGGGAAGGGA AAGACNACAT CNAGACCGCC	180
TTCGCNCCTN GGNATTGTGA GCAGCCTCTG AGACTCATTN ATATNACACT CTCGTNTTTC	240
TTCTTACAAC CCTGCGGNCC GCGCGGTGCG GCTTCTCTG CCTCCGCCG GGTGGACCTG	300
GAGCGCTTGA GCGGTCGGCG CGCCTGGAGC AGCCAGGCGG NCAGTGGACT AGCTGCTGGA	360
CCAGGGAGGT GTGGGAGAGC GGTGGCGGCG GGTACATGCA CGTGAAGCCA TTGCGAGAAC	420
TTTATCCATA AGTATTTCAA TACCGGTAGG GACGGCAAGA GAGGAGGGCG GGATGTGCCA	480
CACATCTTTG ACCTCAGGTT TCTAACGCCT GTTTTCTTTC TGCCCTCTGC AGACAACCCC	540
CGATTGAAAG AACCAGAGAG GCTCTGAGAA ACC	573

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCCCATCGCG CCTTGGGANT GTGAGCNACC ATTGAGACTC ATNAATATAG CACTCGTTTT	60
TCTTCTTGCA ACCCTGCCCN CCGCGCGGTC GCGCTNTCTC TGCCCTCCGC NGGCTGGACC	120
TGGAGCGAGC GCTTGAGCGG TCGGTCGGCG CNCCTGGANC AGCCAGGCGG GCAGTGGACT	180
ACCTNCTGGA CCAGGGACCT GTGGGAGAGC GGTGNCGGCG GGTACATGCA CGTGAAGCCA	240
TTGCGAGAAC TTTATCCATA AGTATTTCAA TGCCGGTAGG GACGGCAAGA GAGGAGGGCG	300
GGATGTNCCA CACATCTTTG ACCTCAGGTT TCTAACGCCT GTTTTCTTTC TGCCCTCTGC	360
AGACATCCCC GATTGAAAGA ACCAGAGAGG CTCTGAGAAA CCTCCGGAAA CTTAGNTCAT	420
CANTCGCCGN AAAA	434

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGAAATTAGA TCATCAGTCA CCGATCCTCC TACAGGGNCA CAACTGNCCC CGCCACAACC	60
CACCCCGNTT TCGTAGTTTT CATTTAGAAA ATAGAGCTTT TAAAAATGTC CTGCCTTTTA	120
ACGTAGATAT ATGCCTTCCC CCACTACCGN AAATGTCCAT TTATATCATN TTTTATATAT	180
TCTTATAAAA ATGTAAAAAA GAAAAACACC GCTTCTGCCT TTCACTGTG TTGGAGTTTT	240
CTGGAGTGAG CACTCACGCC CTAAGCGCAC ATTCATGTGG GCATTTCTTG CGAGCCTCGC	300
AGNCTCCGGA AGCTGTCGAC CTCGAGGGGG GGNCCGGTAC CCAATTGCGC CTATAGTGAG	360
TCGTATTACA ATTCACTGGN CGNCGNTTTT ACAACGTCGG TGGACTGGGA AAACCCCGGN	420
GTTACCCAAC TTTAATCGNC TTGGAGGACA TCCCCCTTTT CGCCAGNTGG GGTATAGNG	480
AAGAGGGCCN CACCNNTCGC CC	502

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:

NGAGTCCACT ATTAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAAACC NTNTTTCAGN 480
GGATTGGNCC ACTACGCNTA NCCATCACCC TATTC 515

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu
1 5 10 15
His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
20 25 30
His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
35 40 45 50
Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
55 60 65
Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
70 75 80 85
Ala Gly Gly Thr

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu

1 5 10 15
 His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
 20 25 30
 His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
 35 40 45 50
 Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
 55 60 65
 Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala
 70 75 80 85
 Thr Gly Asp

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala
 1 5 10 15
 Asp Ser Asn Cys Glu Asp Pro Thr Thr Phe Ser Arg Pro Val His Asp Ala
 20 25 30
 Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala
 35 40 45 50
 Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln
 55 60 65
 Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg Ser Ala Gly Cys Ser
 70 75 80 85



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